

CLAIMS

WE CLAIM:

1. A method of assessing the genotype of an individual comprising the steps of:
 - a) obtaining a nucleic acid sample from an individual to be tested;
 - 5 b) rendering nucleic acid molecules in the nucleic acid sample available for hybridization;
 - c) contacting the sample with at least one allele-specific oligonucleotide that hybridizes to a portion of a gene selected from the group consisting of the genes listed in Table 3, wherein said portion is at least 10 nucleotides in length and comprises a polymorphic site identified in Table 3; and
 - d) identifying hybridization between the allele-specific oligonucleotide and the nucleic acid molecules.
- 15 2. A method according to Claim 1, wherein the sample is contacted with more than one allele-specific oligonucleotide and wherein each allele-specific oligonucleotide hybridizes to a portion of a different gene listed in Table 3.
3. A method according to Claim 1, wherein a central position of the allele-specific oligonucleotide aligns with the polymorphic site of the portion.
- 20 4. A method according to Claim 1, wherein the allele-specific oligonucleotide is a primer and wherein the 3' end of the primer aligns with the polymorphic site of the portion of the gene.

5. A method of analyzing a nucleic acid sample, comprising obtaining the nucleic acid sample from an individual, and determining a base occupying any one of the polymorphic sites listed in Table 3.
6. A method according to Claim 5, wherein the nucleic acid sample is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and wherein the method further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.
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